

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	thermogenic protein	USPAT	ADJ	ON	2004/06/08 20:36



INDEXING CURRENT THROUGH PAT PUB DATE: 25 Nov 2003 (20031125/ED)  
IFIPAT has been reloaded (12/21/2003). See HELP RLOAD for details.

=> S 11 64 THERMOGENIC  
65668 PROTEIN  
37 SKUNK  
450 CABBAGE  
L2 1 (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)  
=> d 12 bib ab  
L2 ANSWER 1 OF 1 IFIPAT COPYRIGHT 2004 IFI ON STN  
AN 10560887 IFIPAT;IFUDB;IFIDB  
TI PLANT THERMOGENIC GENES AND PROTEINS  
INF Ito, Kikuhatsu, Iwate, JP  
IN Ito, Kikuhatsu (JP)  
PA Unassigned Or Assigned To Individual (68000)  
WAENDEROTH, LIND & PONACK, L.L.P., 2033 K STREET N. W., SUITE 800,  
WASHINGTON, DC, 20006-1021, US  
PI 200406105 Al 20040408  
AI US 2003-671628 20030529  
RLI WO 2000-JT3806 20000612 Section 371 PCT Filing UNKNOWN  
DT 2002-9362 20020123 DIVISION  
PRAI JP 1999-157439 19990514  
FI 2004068105 20040408  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
CINN APPLICATION  
GI 6  
GI 8 Figure(s).  
FIG. 1 shows the change of the temperature of the spadix in skunk cabbage and that of ambient temperature with a lapse of time.  
FIG. 2 shows the results of northern blotting, indicating the expression profile of SFUCPA (A) and SFUCPB (B) in the spadix and leaf of skunk cabbage at room temperature (R) and during cold treatment (4 degrees C. for 3 days). The lower figures respectively show the results of ethidium bromide staining of non-decomposed RNA.  
FIG. 3 compares the alignment of amino acid sequences of SFUCPA and SFUCPB, together with potato UCP (AtUPMP) and human UCP. The asterisk (\*) attached under the sequences indicate the same amino acid sequence, and the dot (.) indicates the conservative change in all of the sequences. The boldface indicates the same sequence between SFUCPA and SFUCPB. The gap introduced to optimize the sequence alignment is indicated by a dash (-). The alignment was made using a CLUSTAL W program. The characteristic domains of energy transfer proteins typical of mitochondria are surrounded by a square. The shaded bars (I-VI) above the upper sequence show estimated transmembrane domains.  
FIG. 4 shows a hydrophobic plot of SFUCPA. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TM1 to TM6.

indicated by TM1 to TM4 and TM5.  
FIG. 7 shows a diagrammatic illustration of SFUCPB topology in the mitochondria membrane.  
FIG. 8 shows the results of in vitro translation using respective cDNAs of the genes SFUCPA and SFUCPB as templates. (\*) indicates a control, S a sense RNA, and AS an antisense RNA. The asterisk (\*) indicates a non-specific product and the empty circle denotes the position of a low molecular translated artificial product synthesized from a small ORE. Th inventions of his application include the homologous genes named SFUCPA and SFUCPB which are derived from skunk cabbage cDNA of each gene comprises the base sequence of SEQ ID NO: 1 and 3, respectively.  
The thermogenic proteins, SFUCPA and SFUCPB, are expressed from genes SEQ ID NO: 2 and 4.

=> d his

(FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004)

INDEX 'ADISCTI', 'ADISINSIGHT', 'ADISNEWS', 'AGRICOLA', 'ANABSTR', 'AQUASCI', 'BIOBUSINESS', 'BIOCOMMERCE', 'BIOSIS', 'BIOTCHARBS', 'BIOTECHDS', 'BIOTECHNO', 'CABA', 'CANCERLIT', 'CAPLUS', 'CEARA-VTB', 'CEN', 'CIN', 'CONFSCI', 'CROPP', 'CROPU', 'DISSABS', 'DDFB', 'DDFU', 'DGEDE', 'DRUGDB', 'DRUGMONOG2', ... ENTERED AT 20:39:16 ON 08 JUN 2004

SEA (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

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\* FILE ADISNEWS  
\* FILE BIOCOMMERCE  
\* FILE BIOTCHARBS  
\* FILE BIOTECHDS  
\* FILE BIOTECHNO  
\* FILE CEARA-VTB  
\* FILE CIN  
\* FILE ESBIOBASE  
\* FILE FEDRIP  
\* FILE FORGE  
\* FILE FROSTI  
\* FILE FSTA  
1 FILE IFIPAT  
\* FILE KOSMET  
\* FILE MEDICONF  
\* FILE NTIS  
\* FILE NUTRAEAT  
\* FILE PASCAL  
\* FILE PHARMAM  
QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

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FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

L2 1 S LI

=> LOG  
COST IN U.S. DOLLARS

FULL ESTIMATED COST

SINCE FILE ENTRY  
SESSION 5.91  
7.26

FIG. 5 shows a diagrammatic illustration of SFUCPA topology in the mitochondria membrane.  
FIG. 6 shows a hydrophobic plot of SFUCPB. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are



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OM Protein - Protein search, using sw model

Run on: May 18, 2004, 11:11:47 : Search time 48.3033 Seconds  
(Without alignments)  
1566.356 Million cell updates/sec

Title: US-10-009-962-4

perfect score: 1382

Sequence: 1 MGDHGPRTEISFAGSSRAAF. ....VIMFLTLEQVTKFFIKEVPN 266

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 28254750 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1905:\*

2: geneseqp19905:\*

3: geneseqp20005:\*

4: Geneseqp20015:\*

5: Geneseqp20025:\*

6: Geneseqp20035:\*

7: Geneseqp2003bs:\*

8: geneseqp20045:\*

9: geneseqp20045:\*

10: 595 43.1 308 2 AAW88280

11: 595 43.1 312 2 AAW81587

12: 595 43.1 43.2 2 AAY29835

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19: 594 43.0 309 2 AAY31903

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21: 594 43.0 309 3 AAY45002

22: 594 43.0 309 4 AAY72342

23: 594 43.0 309 5 AAY98501

24: 594 43.0 314 4 AAU09077

25: 593 42.9 308 2 AAY29834

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35: 592 42.8 309 7 ABO14802

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43: 592 42.8 312 3 AAY44193

44: 592 42.8 312 4 AAB74396

45: 592 42.8 312 4 AAE04298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Length	DB ID
1	1382	100.0	AAW73298
2	1344.5	97.3	AAB73297
3	1049	75.9	AAAG4403
4	1031	74.6	AAAG05380
5	1031	74.6	AAAG8337
6	1024.5	74.1	AAAG48300
7	712.5	51.6	AAAG4104
8	597	43.2	AAW81588
9	595	43.1	AAW81595

#### ALIGNMENTS

RESULT 1			
ID	AA	AA	AA
AAB73298	XX	XX	XX
	AC	AC	AC
	DT	DT	DT
			29-MAY-2001 (first entry)
			SFUCPA derived exothermicity relating gene protein #2.
			KW SFUCPA derived exothermicity relating gene; diabetes; obesity; exothermic material; low temperature resistant plant.
			KW KW XX OS OS XX PN JP2000354489-A.

XX DE SFUCPA derived exothermicity relating gene protein #1.  
 XX DE SFUCPA derived exothermicity relating gene; diabetes; obesity;  
 XX KN exothermic material; low temperature resistant plant.  
 XX KN exothermic material; low temperature resistant plant.  
 XX OS Symplocarpus foetidus.  
 XX PN JP200354489-A.  
 XX PD 26-DEC-2000.  
 XX PF 99JJP-00167439.  
 XX PT 14-JUN-1999; 99JJP-00167439.  
 XX PR 14-JUN-1999; 99JJP-00167439.  
 XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX DR WPI: 2001-260368/27.  
 XX DR N-PSDB; AAF77826.  
 XX PT Exothermicity relating genes and proteins, useful in the treatment of  
 PT diabetes and obesity.  
 XX PS Claim 4; Page 10-11; 15pp; Japanese.  
 XX CC The present sequence is a protein encoded by a Symplocarpus foetidus  
 CC (SFUCPA) derived exothermicity Gene. The Gene is useful for  
 CC preparation of low temperature resistant plants, and in the treatment of  
 CC diabetes and obesity. The encoded protein is useful as exothermic  
 CC materials for industrial use.  
 XX SQ Sequence 268 AA:  
 Query Match Score 1382; DB 4; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-138;  
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MGDIGPTEISFASSRAAFACAFELCTPLDTAKRVLQLQKAVTDVVALPKYRML 60  
 Db 1 MGDIGPTEISFASSRAAFACAFELCTPLDTAKRVLQLQKAVTDVVALPKYRML 60  
 Qy 61 GVVATIARESCLSLWKGIVPGLIRHOCFLGRIGLKYEPVKSFYVGDNFVGDPILSKKL 120  
 Db 61 GVVATIARESCLSLWKGIVPGLIRHOCFLGRIGLKYEPVKSFYVGDNFVGDPILSKKL 120  
 Qy 121 AGLTGALAIIVAPTDLVKVRLQSEGKLPGPVRSGALNASTITVKSGLGALWTGL 180  
 Db 121 AGLTGALAIIVAPTDLVKVRLQSEGKLPGPVRSGALNASTITVKSGLGALWTGL 180  
 Qy 181 GPNFARVATINAAELASDQVKQNSRNMGSATKSTPDCPIKTLKNGPLAFYKGFIPN 240  
 Db 181 GPNFARVATINAAELASDQVKQNSRNMGSATKSTPDCPIKTLKNGPLAFYKGFIPN 240  
 Qy 241 FGRIGSNVNIMFLTEQVKKFKEVPN 268  
 Db 241 FGRIGSNVNIMFLTEQVKKFKEVPN 268  
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 ID AAB73297  
 ID AAB73297 standard; protein: 303 AA.  
 XX AC AAB73297;  
 XX DT 29-MAY-2001 (first entry)  
 XX DR 2006 SRMNGDSAYKSTDFCFIKTLKNDGFLAFYKGFIPNFRGSNNVZMFTLEQVKKFKE 265  
 XX DR 241 SRMNGDSAYKSTDFCFIKTLKNDGFLAFYKGFIPNFRGSNNVZMFTLEQVKKFKE 300  
 XX PR 14-JUN-1999; 99JJP-00167439.  
 XX DR 2001-260368/27.  
 XX DR N-PSDB; AAF77825.  
 XX PT Exothermicity relating genes and proteins, useful in the treatment of  
 PT diabetes and obesity.  
 XX SQ Sequence 303 AA:  
 Query Match Score 1344.5; DB 4; Length 303;  
 Best Local Similarity 88.1%; Pred. No. 9.7e-134;  
 Matches 267; Conservative 0; Mismatches 1; Indels 35; Gaps 1;  
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 Db 1 MGDHCPRTIEISFASSRAAFACAFELCTPLDTAKRVLQLQKAVTDVVALPKYRML 60  
 Qy 61 GTVATIAREGGSALWKGIVPGLIRHOCFLGRIGLKYEPVKSFYVGDNFVGDPILSKKL 120  
 Db 61 GTVATIAREGGSALWKGIVPGLIRHOCFLGRIGLKYEPVKSFYVGDNFVGDPILSKKL 120  
 Qy 121 AGLTGALAIIVAPTDLVKVRLQSEGKLPGPVRSGALNASTITVKSGLGALWTGL 180  
 Db 121 AGLTGALAIIVAPTDLVKVRLQSEGKLPGPVRSGALNASTITVKSGLGALWTGL 180  
 Qy 181 GPNFARVATINAAELASDQVKQNSRNMGSATKSTPDCPIKTLKNGPLAFYKGFIPN 240  
 Db 181 GPNFARVATINAAELASDQVKQNSRNMGSATKSTPDCPIKTLKNGPLAFYKGFIPN 240  
 Qy 241 FGRIGSNVNIMFLTEQVKKFKEVPN 268  
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 XX PR 14-JUN-1999; 99JJP-00167439.  
 XX DR 2006 SRMNGDSAYKSTDFCFIKTLKNDGFLAFYKGFIPNFRGSNNVZMFTLEQVKKFKE 265  
 XX DR 241 SRMNGDSAYKSTDFCFIKTLKNDGFLAFYKGFIPNFRGSNNVZMFTLEQVKKFKE 300

Qy      266 VPN 268  
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 Db      301 VPN 303

Search completed: May 18, 2004, 11:18:52  
 Job time : 49.343 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:57 ; Search time 15.4886 Seconds  
 (without alignments)  
 893.286 Million cel1 updates/sec

Title: US-10-009-962-4  
 Perfect score: 1382  
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Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs. 5162571 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 4: /cgnd\_6\_ptodata/2/iaa/6B\_COMB.pep:  
 5: /cgnd\_6\_ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /cgnd\_6\_ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	595	43.1	432	2	US-08-937-466-4		Sequence 4, App1
2	595	43.1	432	2	US-09-172-528-4		Sequence 4, App1
3	595	43.1	432	3	US-09-318-199-4		Sequence 4, App1
4	595	43.1	432	3	US-09-503-577-4		Sequence 4, App1
5	594	43.0	309	4	US-09-743-847-4		Sequence 4, App1
6	594	43.0	309	4	US-10-001-051B-2		Sequence 2, App1
7	593	42.9	308	2	US-08-937-466-2		Sequence 2, App1
8	593	41.9	308	2	US-09-172-528-2		Sequence 2, App1
9	593	42.9	308	3	US-09-318-199-2		Sequence 2, App1
10	593	42.9	308	3	US-09-503-577-2		Sequence 2, App1
11	592	42.8	309	1	US-08-518-878B-51		Sequence 51, App1

12      42.8      US-08-807-861A-51      Sequence 51, Appli  
 13      42.8      US-08-870-868A-51      Sequence 51, Appli  
 14      42.8      US-09-210-681-51      Sequence 51, Appli  
 15      42.8      US-08-946-719A-51      Sequence 51, Appli  
 16      42.8      US-09-547-983-51      Sequence 51, Appli  
 17      42.8      US-09-142-565-2      Sequence 2, Appli  
 18      42.8      US-09-308-457-2      Sequence 2, Appli  
 19      42.8      US-09-423-410-4      Sequence 4, Appli  
 20      42.8      US-08-518-878B-56      Sequence 56, Appli  
 21      42.8      US-08-410-868A-56      Sequence 56, Appli  
 22      52.1      US-09-243-847-5      Sequence 5, Appli  
 23      54.2      US-09-243-847-3      Sequence 3, Appli  
 24      53.2.5      PCT-US94-05799-1      Sequence 1, Appli  
 25      51.6      US-08-807-861A-56      Sequence 56, Appli  
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 27      51.6      US-08-946-719A-56      Sequence 56, Appli  
 28      51.6      US-09-547-983-56      Sequence 56, Appli  
 29      50.1      US-08-294-522B-36      Sequence 36, Appli  
 30      49.8      US-08-518-878B-37      Sequence 37, Appli  
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 35      49.8      US-09-547-983-37      Sequence 4, Appli  
 36      49.6      US-08-808-457-4      Sequence 6, Appli  
 37      49.6      US-09-443-410-6      Sequence 6, Appli  
 38      46.9      US-08-937-466-6      Sequence 6, Appli  
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 40      46.9      US-09-318-199-6      Sequence 6, Appli  
 41      46.9      US-09-503-579-6      Sequence 6, Appli  
 42      41.5      US-09-150-558-2      Sequence 2, Appli  
 43      41.0.5      US-09-743-847-2      Sequence 2, Appli  
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Job time : 16.4886 secs

OM protein - protein search, using SW model  
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 (without alignments)  
 2037.01 Million cell updates/sec

#### SUMMARIES

Result No.	Score	Query ID	Match Length	DB ID	Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins

; FILE REFERENCE: 2003-138A/WMC/00653

; CURRENT APPLICATION NUMBER: US/10/671,628

; CURRENT FILING DATE: 2003-09-29

; PRIORITY APPLICATION NUMBER: 10/039,962

; PRIORITY FILING DATE: 2002-01-23

; PRIORITY APPLICATION NUMBER: PCT/JP00/03806

; PRIORITY FILING DATE: 2000-06-12

; PRIORITY APPLICATION NUMBER: JP11-167439

; PRIORITY FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 4

; LENGTH: 268

; TYPE: PRT

; ORGANISM: Symplocarpus foetidus

; US-10-671-628-4

Query Match 100.0% Score 1382; DB 12; Length 268;

Best Local Similarity 100.0%; Pred. No. 1..e-136;

Indels 0; Gaps 0;

Matches 268; Conservative 0; Mismatches 0;

Appli Sequence 1, Appli

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Sequence 241, Appli

Sequence 242, Appli

Sequence 243, Appli

; PRIOR APPLICATION NUMBER: JP11-167439  
 ; PRIOR FILING DATE: 1999-06-14  
 ; NUMBER OF SEQ ID NCS: 12  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 303  
 ; TYPE: PRT  
 ; ORGANISM: *Symplocarpus foetidus*  
 US-10-671-628-2

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OM protein - protein search, using sw model  
 Run on: May 18, 2004, 11:16:07 ; Search time 13.612 Seconds  
 {without alignments}  
 1893.978 Million cell updates/sec

Query Match 97.3%; Score 1344.5; DB 12; Length 303;  
 Best Local Similarity 88.1%; Pred. No. 1.le-12;  
 Matches 267; Conservative 0; Mismatches 1; Indels 35; Caps 1;  
 SEQ ID NO: 2  
 ; LENGTH: 303  
 ; TYPE: PRT  
 ; ORGANISM: *Symplocarpus foetidus*  
 US-10-671-628-2

```

Title: US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDRGPRTEISFAGSSAAFAACEAELCTIPDLOTAKRQLQKAVTGVALPKYRGMV 60
Scoring table: BLOSUM62
gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_78:*
  1: Pirl:*
  2: Pir2:*
  3: Pir3:*
  4: Pir4:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1121	81.1	306	2	T07793		uncoupling protein
2	1049	75.9	306	2	T42570		uncoupling protein
3	1040	75.3	306	2	T52024		uncoupling protein
4	592	42.8	312	2	JC522		uncoupling protein
5	542	39.2	307	2	G01858		uncoupling protein
6	518	37.5	307	2	S32468		uncoupling protein
7	518	37.5	307	2	A22294		mitochondrial uncoupling protein
8	516	37.3	306	2	A31106		uncoupling protein
9	504.5	36.5	306	2	A32446		uncoupling protein
10	503.5	36.4	288	2	S03603		F7A19.22 protein -
11	423.5	30.6	305	2	H86744		hypothetical protein
12	421.5	30.5	313	2	D84113		uncoupling protein
13	419.5	30.4	313	2	T05577		

C;Keywords: mitochondrial

14	410.5	29.7	343	2	T1553	
15	409.5	29.6	345	2	JC7553	
16	360	26.0	323	2	T2559	
17	344	24.9	302	2	S65040	
18	336	24.5	302	2	S65042	
19	334.5	24.2	314	2	A36305	
20	331	24.0	297	2	T07405	
21	324.5	23.5	314	2	A56650	
22	317.5	23.0	290	2	S44091	
23	291.5	21.1	282	2	T49528	
24	275	19.9	298	2	S51351	
25	274.5	19.9	320	2	T37603	
26	273.5	19.8	324	2	S25557	
27	270	19.5	331	2	T51899	
28	266.5	19.3	322	2	S57116	
29	247.5	17.9	311	2	A45591	
30	246.5	17.8	415	2	T48571	
31	241.5	17.5	312	2	R88567	
32	235.5	17.0	309	2	T48156	
33	232.5	16.8	301	2	S51132	
34	232.5	16.8	311	2	G01789	
35	226.5	16.4	373	2	S4451	
36	226	16.4	479	2	T48871	
37	224.5	16.2	702	2	T16533	
38	223.5	16.2	298	1	XWBO	
39	223.5	16.2	381	2	T51158	
40	221	16.0	300	2	T15206	
41	217.5	15.7	298	2	B43646	
42	215.5	15.6	93	2	S16082	
43	215.5	15.6	299	2	S44554	
44	212.5	15.4	358	2	T09109	
45	211.5	15.3	313	2	T23207	

#### ALIGNMENTS

#### RESULT 1

T07793 uncoupling protein (clone StUCP7), mitochondrial - potato

C;Species: Solanum tuberosum (potato)

C;Date: 1-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000

C;Accession: T07793

R:Laloi, M.; Klein, M.; Riesmeier, J.W.; Mueller-Roeber, B.; Fleury, C.;

Bouillaud, F.; Ricquier, D.

Nature 389, 135-136, 1997

A;Title: A Plant cold-induced uncoupling protein.

A;Reference number: Z161336; PMID:97441001; PMID:9296489

A;Accession: T07793

A>Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-306 <LAL>

A;Cross-references: EMBL:Y11220; NID:G2398828; PID:CAA72107.1; PID:92398829

A;Experimental source: cv. Desiree

C;Generics:

A;Genome: nuclear

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

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#### OM Protein - protein search, using sw model

Run On: May 18, 2004, 11:12:22 ; Search time 9:38:704 Seconds

(without alignment)

1486.603 Million cell updates/sec

Title: US-10-009-9624

Perfect score: 1382

Sequence: 1 MGDHGPRTEISFGSSRAAF.....VIMPLTLEQYKKEFIKEVPN 268

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched:

141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	601	43.5	310	1 UCP2_CYPCA	Q9W725 Cyprinus carpio
2	600.5	43.5	311	1 UCP3_BOVIN	Q7792 Bos taurus
3	597.5	43.2	311	1 UCP3_CANFA	Q9z219 Canis familiaris
4	595	43.1	308	1 UCP3_MOUSE	P56501 Mus musculus
5	595	43.1	309	1 UCP2_MOUSE	P70406 Mus musculus
6	595	43.1	310	1 UCP2_BREARE	Q9W720 Brachydanio
7	594	43.0	309	1 UCP2_HUMAN	P53851 Homo sapiens
8	593	42.9	308	1 UCP3_RAT	P56199 Rattus norvegicus
9	593	42.9	309	1 UCP2_PIG	Q97562 Sus scrofa
10	592	42.8	309	1 UCP2_RAT	P56500 Rattus norvegicus
11	592	42.8	312	1 UCP3_HUMAN	P55916 Homo sapiens
12	587	42.5	309	1 UCP2_CANFA	Q9njj1 Canis familiaris
13	583	42.2	308	1 UCP3_PIG	Q97649 Sus scrofa
14	541	39.1	307	1 UCP1_HUMAN	P23874 Homo sapiens
15	518	37.5	306	1 UCP1_MESAU	P04575 Mesocricetus auratus
16	518	37.5	306	1 UCP1_RAT	P04633 Rattus norvegicus
17	516	37.3	306	1 UCP1_MOUSE	P12242 Mus musculus

Search completed: May 18, 2004, 11:19:24  
 Job time : 10:38 secs

1.8	509.5	36.9	306	1 UCPI_RABBIT	P14271 Oryctolagus cuniculus
1.9	503.5	36.4	288	1 UCPI_BOVIN	P10851 Bos taurus
2.0	43.6	31.5	323	1 UCPI_HUMAN	Q95487 Homo sapiens
2.1	410.5	29.7	325	1 UCPI_HUMAN	Q9z238 Homo sapiens
2.2	406.5	29.4	325	1 UCPS_MOUSE	Q9zb22 Mus musculus
2.3	366	26.5	287	1 DIC_HUMAN	P32332 Saccharomyces cerevisiae
2.4	351.5	25.4	287	1 DIC_MOUSE	P32333 Saccharomyces cerevisiae
2.5	334.5	24.2	313	1 M2OM_BOVIN	P22232 Bos taurus
2.6	333.5	24.1	313	1 M2OM_MOUSE	Q9cb62 Mus musculus
2.7	324.5	23.5	313	1 M2OM_HUMAN	Q92978 Homo sapiens
2.8	318.5	23.0	313	1 M2OM_RAT	P297700 Rattus norvegicus
2.9	273.5	19.8	324	1 OACI_YEAST	P32332 Saccharomyces cerevisiae
3.0	266.5	19.3	322	1 SFC1_YEAST	P32333 Saccharomyces cerevisiae
3.1	247.5	17.9	311	1 TXTP_RAT	P32059 Rattus norvegicus
3.2	241.5	17.5	312	1 TXTP_CABEL	P34519 Caenorhabditis elegans
3.3	232.5	16.8	311	1 TXTP_HUMAN	P53007 Homo sapiens
3.4	231.5	16.8	311	1 TXTP_BOVIN	P29110 Bos taurus
3.5	226.5	16.4	375	1 YIA6_YEAST	P40556 Saccharomyces cerevisiae
3.6	226	16.4	675	1 CMC2_HUMAN	Q9uj10 Homo sapiens
3.7	224.5	16.2	702	1 CMC1_CABEL	Q2113 Caenorhabditis elegans
3.8	224	16.2	299	1 ODC_HUMAN	Q9bq18 Homo sapiens
3.9	223.5	16.2	297	1 ADT1_BOVIN	P02722 Bos taurus
4.0	222.5	16.1	316	1 MFTC_MOUSE	Q9bx98 Mus musculus
4.1	222	16.1	300	1 MCAT_ARATH	Q93xm7 Arabidopsis thaliana
4.2	220	15.9	676	1 CMC2_MOUSE	Q9qxx4 Mus musculus
4.3	219.5	15.9	678	1 CMC1_HUMAN	Q75746 Homo sapiens
4.4	219	15.8	298	1 ODC_RAT	Q9pj33 Rattus norvegicus
4.5	217.5	15.7	298	1 ADT3_BOVIN	P32007 Bos taurus

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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:11:47 ; Search time 54.6567 Seconds  
(without alignments)  
1566.356 Million cell updates/sec

Title: US-10-009-962-2

Perfect score: 1561

Sequence: MCDHGPRTEISFAGSSRAAF.....VIMFLTLEQVKKKFFKEVVPN 303

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1561	AAB7297	303	4	Aab7327 SFUCpa de
2	1344.5	86.1	268	4	Aab73298 SFUCpa de
3	1234.5	79.0	306	3	Aag41403 Arabidops
4	1206.5	77.3	305	3	Aag5380 Arabidops
5	1206.5	77.3	305	3	Aag48337 Arabidops
6	1190	76.2	318	3	Aag48300 Arabidops
7	896	57.4	212	3	Aag41404 Arabidops
8	748	47.9	177	3	Aag41405 Arabidops
9	685.5	43.9	308	2	Aaw81959 Mouse unc

10	685.5	43.9	308	2	AAW88280 Mouse unc
11	685.5	43.9	432	2	AAY29855
12	685.5	43.9	432	2	AAW85117
13	685.5	43.9	432	3	AAY77453
14	685.5	43.9	432	4	AAB04730 Mouse unc
15	683.5	43.8	308	2	AAY29834
16	683.5	43.8	308	2	AAW85116 A murine
17	683.5	43.8	308	3	Aay77452 Murine mi
18	683.5	43.8	308	4	AAB04729 Mouse unc
19	682.5	43.7	397	2	AAW81596 Protein e
20	680.5	43.6	403	2	AAW81583
21	678.5	43.5	312	2	AAW81587 Human unc
22	677.5	43.4	309	2	AAW89166 Human res
23	677.5	43.4	309	2	AAY23352 UCP2 amin
24	677.5	43.4	309	5	AAU88901 Human unc
25	677.5	43.4	309	7	ADE54389 Rat Prote
26	675.5	43.3	312	2	Aaw83379 Human unc
27	675.5	43.3	312	2	Aaw68197 Human unc
28	675.5	43.3	312	2	Aaw85667 Human UCP
29	675.5	43.3	312	2	Aaw88279 Human unc
30	675.5	43.3	312	2	AAY81904 Human unc
31	675.5	43.3	312	3	AAY84600 Amino aci
32	675.5	43.3	312	3	AAY4253 Human mit
33	675.5	43.3	312	4	AAB74296 Human UCP
34	675.5	43.3	312	4	AAE04298 Human unc
35	675.5	43.3	312	4	AAB8050 Amino aci
36	675.5	43.3	312	5	Abbb81610 UCP3L pro
37	675.5	43.3	312	5	Aae19348 Human mit
38	675.5	43.3	312	7	ADE54391 Human pro
39	674.5	43.2	309	2	AAY28351 UCP2 amino
40	674.5	43.2	309	2	Aay31903 Human unc
41	674.5	43.2	309	3	AAY44292 Human unc
42	674.5	43.2	309	3	AAY50022 Tularik h
43	674.5	43.2	309	4	Aay77234 Human unc
44	674.5	43.2	314	4	Aau09077 Human unc
45	672.5	43.1	309	2	Aaw24000 Complete

#### ALIGNMENTS

RESULT 1	
ID	AAB73297
DT	29-MAY-2001 (first entry)
XX	sfUCpa derived exothermicity relating gene protein #1.
AC	AAB73297;
XX	sfUCpa derived exothermicity relating gene: diabetes: obesity:
XX	exothermic material; low temperature resistant plant.
XX	sfUCpa derived exothermicity relating gene: diabetes: obesity:
XX	exothermic material; low temperature resistant plant.
OS	Symplocarpus foetidus.
XX	sfUCpa derived exothermicity relating gene: diabetes: obesity:
XX	exothermic material; low temperature resistant plant.
PN	JP2000354489-A.
XX	26-DEC-2000.

DT	29-MAY-2001	(first entry)
XX	XX	sfucpa derived exothermicity relating gene protein #2.
DE	XX	sfucpa derived exothermicity relating gene; diabetes; obesity;
KW	KW	exothermic material; low temperature resistant plant.
PA	XX	Symplocarpus foetidus.
WPI:	WPI ; DR	OS
XX	XX	JP2000354489-A.
PT	PT	PN
PT	PT	XX
PT	PT	XX
XX	XX	26-DEC-2000.
PS	PS	PD
XX	PF	PF
CC	CC	14-JUN-1999 ; 99JP-00167439.
CC	CC	14-JUN-1999 ; 99JP-00167439.
CC	CC	14-JUN-1999 ; 99JP-00167439.
CC	CC	PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
CC	CC	PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX	XX	XX
XX	XX	WPI : 2001-260368/27.
XX	DR	DR
XX	N-PSDB ; AAF77826.	N-PSDB ; AAF77826.
Claim 3; Page 7-8; 15pp; Japanese.	Exothermicity relating Genes and proteins, useful in the treatment of diabetes and obesity.	Claim 4; Page 10-11; 15pp; Japanese.
The present sequence is a protein encoded by a Symplocarpus foetidus (sfucpa) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment of diabetes and obesity. The encoded protein is useful as exothermic materials for industrial use.	Exothermicity relating Genes and proteins, useful in the treatment of diabetes and obesity.	Exothermicity relating Genes and proteins, useful in the treatment of diabetes and obesity.
Sequence 303 AA:	Query Match 100.0%; Score 1561; DB 4; Length 303; Best Local Similarity 100.0%; Pred. No. 6.5e-151; Mismatches 0; Indels 0; Gaps 0; Matches 303; Conservative	Query Match 86.1%; Score 1344.5; DB 4; Length 266; Best Local Similarity 88.1%; Pred. No. 7.8e-129; Mismatches 0; Indels 35; Gaps
Qy 1 MGDHGPRTESFAGSSRAAAACFAELCTPLDTAKVRLQLQQKAVTCDDVIALPKYRGM 60	XX	XX
Db 1 MGDHGPRTESFAGSSRAAAACFAELCTPLDTAKVRLQLQQKAVTCDDVIALPKYRGM 60	CC	CC
Qy 61 GTVATIAAREEGLSALWKG1 VIGLARQLFGRLGRLGRLGRLGRLGRLGRLGRLG 120	CC	The present sequence is a protein encoded by a <i>Symplocarpus foetidus</i> (sfucpa) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment of diabetes and obesity. The encoded protein is useful as exothermic materials for industrial use.
Db 61 GTVATIAAREEGLSALWKG1 VIGLARQLFGRLGRLGRLGRLGRLGRLGRLG 120	CC	CC
Qy 121 AGLTGALAIIVANPTDLVKYRLQSEGKLPPCPVPRYSGALNAYSTIVRKEGLGALWTGL 180	XX	XX
Db 121 AGLTGALAIIVANPTDLVKYRLQSEGKLPPCPVPRYSGALNAYSTIVRKEGLGALWTGL 180	CC	CC
Qy 181 GPNTARNIINAAELASYDQVQTQTLKLPGFSDNFTHILAGLGAFFAVCIGSPVYDNK 240	Db	1 MGDHGPRTESFAGSSRAAAACFAELCTPLDTAKVRLQLQQKAVTCDDVIALPKYRGM 60
Db 181 GPNTARNIINAAELASYDQVQTQTLKLPGFSDNFTHILAGLGAFFAVCIGSPVYDNK 240	Db	1 MGDHGPRTESFAGSSRAAAACFAELCTPLDTAKVRLQLQQKAVTCDDVIALPKYRGM 60
Qy 241 SRMIGDSAYKSTEDCFIKTLDLQKLLGKIPNFGRLGSGNVIMETLQKKEFFIKE 300	Qy	61 GTVATIAAREEGLSALWKG1 VIGLARQLFGRLGRLGRLGRLGRLGRLGRLG 12
Db 241 SRMIGDSAYKSTEDCFIKTLDLQKLLGKIPNFGRLGSGNVIMETLQKKEFFIKE 300	Db	61 GTVATIAAREEGLSALWKG1 VIGLARQLFGRLGRLGRLGRLGRLGRLGRLG 12
Qy 341 VPN 303	Qy	121 AGLTGALAIIVANPTDLVKYRLQSEGKLPPCPVPRYSGALNAYSTIVRKEGLGALWTGL 18
Db 341 VPN 303	Db	121 AGLTGALAIIVANPTDLVKYRLQSEGKLPPCPVPRYSGALNAYSTIVRKEGLGALWTGL 18
RESULT 2	181 GPNTARNIINAAELASYDQVQTQTLKLPGFSDNFTHILAGLGAFFAVCIGSPVYDNK 24	-----
AB77298	181 GPNTARNIINAAELASYDQVQTQTLKLPGFSDNFTHILAGLGAFFAVCIGSPVYDNK 24	MK 20
ID AAB73298 standard; protein; 268 AA.	Db 181 GPNTARNIINAAELASYDQVQTQTLKLPGFSDNFTHILAGLGAFFAVCIGSPVYDNK 24	AC AC
XX	Qy 241 SRMIGDSAYKSTEDCFIKTLDLQKLLGKIPNFGRLGSGNVIMETLQKKEFFIKE 30	30

Db 206 SRMNGDSAYRSTPDCFIKTLKNDGPIAFYRGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 265  
 Qy 301 VPN 303  
 |||  
 Db 266 VPN 268

Search completed: May 18, 2004, 11:16:51  
 Job time : 56.657 secs

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OM protein - protein search, using sw model  
 Run on: May 18, 2004, 11:16:57 ; Search time 17.5114 Seconds  
 (without alignments)  
 893.286 Million cell updates/sec

Title: US-10-009-962-2  
 Perfect score: 1561  
 Sequence: 1 MGDHGPRTEISFGSSRAAF.....VINFILEQVKKFKEVKPVN 303

Scoring table: BLOSUM62  
 Gapcp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

POST-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
 1: /cgri2\_6/prodata/2/iaaa/5A\_CONB.pep:/\*  
 2: /cgri2\_6/prodata/2/iaaa/5B\_CONB.pep:/\*  
 3: /cgri2\_6/prodata/2/iaaa/6A\_CONB.pep:/\*  
 4: /cgri2\_6/prodata/2/iaaa/6B\_CONB.pep:/\*  
 5: /cgri2\_6/prodata/2/iaaa/PCTUS\_CONB.pep:/\*  
 6: /cgri2\_6/prodata/2/iaaa/backfile1.pep:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	685.5	43.9	432	2	US-08-937-466-4	Sequence 4, Appli
2	685.5	43.9	432	2	US-09-172-528-4	Sequence 4, Appli
3	685.5	43.9	432	3	US-09-318-199-4	Sequence 4, Appli
4	685.5	43.9	432	3	US-09-503-579-4	Sequence 4, Appli
5	683.5	43.8	308	2	US-08-937-466-2	Sequence 2, Appli
6	683.5	43.8	308	2	US-09-172-528-2	Sequence 2, Appli
7	682.5	43.8	308	3	US-09-318-199-2	Sequence 2, Appli
8	683.5	43.8	308	3	US-09-503-579-2	Sequence 2, Appli
9	677.5	43.4	309	4	US-10-001-051B-2	Sequence 2, Appli
10	675.5	43.3	312	3	US-09-142-555-2	Sequence 2, Appli
11	675.5	43.3	312	4	US-09-808-457-2	Sequence 2, Appli

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 OM protein - protein search, using sw model  
 Run on: May 18, 2004, 11:20:53 ; Search time 41.3905 Seconds  
 (without alignments)  
 2037.017 Million cell updates/sec

Job ID	Score	Length	DB ID	Description
12	43.3	4	US-09-433-10-4	Sequence 4, Appli
13	43.2	309	4	US-09-743-847-4
14	43.1	309	1	US-08-518-879B-51
15	43.1	309	2	US-08-807-861A-51
16	43.1	309	2	US-08-470-868A-51
17	43.1	309	3	US-09-210-681-51
18	43.1	309	3	US-08-946-719A-51
19	43.1	309	4	US-09-547-883-51
20	43.0	299	1	US-08-518-878B-56
21	43.0	299	2	US-08-470-868A-56
22	42.0	310	4	US-09-743-847-5
23	414.5	39.4	307	4 US-09-743-847-3
24	38.8	306	5	PCT-US09-09799-1
25	37.8	307	2	US-08-807-861A-56
26	37.8	307	3	US-09-210-681-56
27	37.8	307	3	US-08-946-719A-56
28	37.8	307	4	US-09-547-883-56
29	37.1	275	4	US-09-808-857-4
30	579.5	37.1	275	4 US-09-423-110-6
31	569.5	36.5	303	1 US-08-294-522B-36
32	566.5	36.3	303	1 US-08-518-878B-37
33	566.5	36.3	303	2 US-08-807-861A-37
34	566.5	36.3	303	2 US-08-470-868A-37
35	566.5	36.3	303	3 US-09-210-681-37
36	566.5	36.3	303	3 US-09-946-719A-37
37	566.5	36.3	303	4 US-09-547-883-37
38	546.5	35.0	256	2 US-08-937-866-6
39	546.5	35.0	256	2 US-09-172-328-6
40	546.5	35.0	256	3 US-09-318-199-6
41	546.5	35.0	256	3 US-09-503-579-6
42	489.5	31.4	291	4 US-09-501-558-2
43	481	30.8	290	4 US-09-743-847-2
44	481	30.8	335	4 US-08-470-873-118
45	362.5	23.2	293	4 US-09-501-558-4

Search completed: May 18, 2004, 11:22:16  
 Job time : 18.5114 secs

Published\_Applications\_AA:  
 Database :  
 Listing first 45 summaries  
 Total number of hits satisfying chosen parameters: 1145568  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Searched: 1145568 seqs, 278261457 residues  
 Perfect score: 1561  
 Sequence: 1 MGHDGRTEISFRGSSRAAF.....VINFILEQVKKFFIKEVPN 303

Scoring table: BLOSUM62  
 Gapext 0.5  
 Gapop 10.0

Sequence 1, Appli  
 Sequence 2, Appli  
 Sequence 3, Appli  
 Sequence 4, Appli  
 Sequence 5, Appli  
 Sequence 6, Appli  
 Sequence 7, Appli  
 Sequence 8, Appli  
 Sequence 9, Appli  
 Sequence 10, Appli  
 Sequence 11, Appli  
 Sequence 12, Appli  
 Sequence 13, Appli  
 Sequence 14, Appli  
 Sequence 15, Appli  
 Sequence 16, Appli  
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 Sequence 34, Appli  
 Sequence 35, Appli  
 Sequence 36, Appli  
 Sequence 37, Appli  
 Sequence 38, Appli  
 Sequence 39, Appli  
 Sequence 40, Appli  
 Sequence 41, Appli  
 Sequence 42, Appli  
 Sequence 43, Appli  
 Sequence 44, Appli  
 Sequence 45, Appli

Summary 1: /cgn2\_6\_ptodata/1/pubpaas/US09\_PUBCOMB.pep:\*

Summary 2: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 3: /cgn2\_6\_ptodata/1/pubpaas/US06\_PUBCOMB.pep:\*

Summary 4: /cgn2\_6\_ptodata/1/pubpaas/US07\_PUBCOMB.pep:\*

Summary 5: /cgn2\_6\_ptodata/1/pubpaas/US08\_PUBCOMB.pep:\*

Summary 6: /cgn2\_6\_ptodata/1/pubpaas/US09\_PUBCOMB.pep:\*

Summary 7: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 8: /cgn2\_6\_ptodata/1/pubpaas/US08\_PUBCOMB.pep:\*

Summary 9: /cgn2\_6\_ptodata/1/pubpaas/US09\_PUBCOMB.pep:\*

Summary 10: /cgn2\_6\_ptodata/1/pubpaas/US09\_PUBCOMB.pep:\*

Summary 11: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 12: /cgn2\_6\_ptodata/1/pubpaas/US06\_PUBCOMB.pep:\*

Summary 13: /cgn2\_6\_ptodata/1/pubpaas/US07\_PUBCOMB.pep:\*

Summary 14: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 15: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 16: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 17: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Summary 18: /cgn2\_6\_ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DOCUMENTS

RESULT 1	US-10-671	Sequenc	Publica	GENERAL	APPLIC	TITLE	FILE R	CURRENT
----------	-----------	---------	---------	---------	--------	-------	--------	---------

; PRIOR FILING DATE: 2000-06-12  
 ; PRIOR APPLICATION NUMBER: JP11-167439  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 268  
 ; TYPE: PTI  
 ; ORGANISM: Symplocarpus foetidus  
 ; US-10-671-628-4

Query Match Score 1344.5; DB 12; Length 268;  
 Best Local Similarity 88.1%; Pred. No. 2.3e-128;  
 Matches 267; Conservative 0; Mismatches 1; Indels 35; Gaps 1;

Qy	1	MGDHGPRTRBISFGSSRAAAFAACFAELCIPIDLTAKRQLQQKAVTGDVALPKYRGM	60
Db	1	MGDHGGRTEISFGSSRAAAFAACFAELCIPIDLTAKRQLQQKAVTGDVALPKYRGM	60
Qy	61	GTVATIAREGSALWKGIVPGHRCQLFGLGRLIGYEPVKSFTYQDNTVGDPLSKKL	120
Db	61	GTVATIAREGSALWKGIVPGHRCQLFGLGRLIGYEPVKSFTYQDNTVGDPLSKKL	120
Qy	121	AGTTGALIAIVNPTDLYVKRLQSCKLPPGVPRRYSGALNAYSTIVKEGGALWTGL	180
Db	121	AGTTGALIAIVNPTDLYVKRLQSCKLPPGVPRRYSGALNAYSTIVKEGGALWTGL	180
Qy	181	GPMIARNALINAAELASIVOKTILKPGFSDNITHIAGLGAFFAVICSPVDWK	240
Db	181	GPMIARNALINAAELASIVOKTILKPGFSDNITHIAGLGAFFAVICSPVDWK	240
Qy	241	SRMGDSAYKSTPDCFITKLNDGLAFLIKGFIPNFGRLGSNNVINFITLEQVKKFKE	300
Db	206	SRMGDSAYKSTPDCFITKLNDGLAFLIKGFIPNFGRLGSNNVINFITLEQVKKFKE	265
Qy	301	VPN 303	
Db	266	VPN 268	

Search completed: May 18, 2004, 11:30:31  
 Job time : 42.3905 secs

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OM protein - protein search, using SW model

Run on: May 18, 2004, 11:16:07 ; Search time 15.3888 Seconds  
 (without alignments)  
 1893.978 Million cell updates/sec

Title: US-10-009-962-2  
 Perfect score: 1561  
 Sequence: 1 MGDHGPRTRBISFGSSRAAF.....VIMFITLEQVKKFKEVPN 303

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1294.5	82.9	306	2	T07793		uncoupling protein
2	1222.5	79.0	306	2	T47510		uncoupling protein
3	1223.5	78.4	306	2	TS2024		uncoupling protein
4	675.5	43.3	312	2	JC5522		uncoupling protein
5	614.5	39.4	307	2	G01958		uncoupling protein
6	521.5	37.9	307	2	A26294		uncoupling protein
7	589.5	37.8	306	2	A31106		mitochondrial uncoupling protein
8	583.5	37.4	307	2	S34268		uncoupling protein
9	579	37.1	306	2	A2446		uncoupling protein
10	574	36.8	288	2	S03603		hypothetical protein
11	520	33.3	313	2	D84613		hypothetical protein
12	510	32.7	313	2	T05577		uncoupling protein
13	508	32.5	305	2	H86274		F7A19.22 protein -

14	483	30.9	343	2	T15253	hypothetical prote			
15	481	30.8	325	2	JC7553	brain mitochondria			
16	441.5	28.3	323	2	T25459	hypothetical prote			
17	470	26.9	314	2	A36305	2-oxoglutarate/mal			
18	409	26.2	314	2	A56650	2-oxoglutarate car			
19	382	24.5	290	2	S44091	oxoglutarate/malat			
20	379	24.3	282	2	T49628	probable dicarboxy			
21	361.5	23.2	297	2	T07405	oxoglutarate/malat			
22	358.5	23.0	302	2	S65040	2-oxoglutarate/mal			
23	353.5	22.6	302	2	S65042	2-oxoglutarate/mal			
24	337.5	21.6	298	2	S51351	hypothetical prote			
25	321	20.6	320	2	T37603	probable oxaloacet			
26	319	20.4	324	2	S25457	mitochondrial unco			
27	318.5	20.4	331	2	T51899	probable 2-oxoglut			
28	302	19.3	322	2	S51216	probable carrier?			
29	277	17.7	309	2	T48156	hypothetical prote			
30	275	17.6	415	2	T48171	protein K11H3_3 [i			
31	273	17.5	312	2	H88567	ADP,ATP carrier pr			
32	266	17.0	301	2	S51132	hypothetical protein			
33	258.5	16.6	300	2	T15206	peroxisomal Ca-dep			
34	258.5	16.6	479	2	T49871	citrate transport			
35	257	16.5	311	2	G01789	tricarboxylate tra			
36	257	16.5	311	2	A46535	citrate transport			
37	254	16.3	299	2	S44554	hypothetical prote			
38	252	16.1	381	2	T51158	probable membrane			
39	251	16.1	373	2	S48451	probable membrane			
40	246.5	15.8	310	2	S69050	probable tricarbox			
41	245.5	15.7	291	2	T37929	hypothetical prote			
42	245	15.7	702	2	T16533	hypothetical prote			
43	244	15.6	313	2	T23207	hypothetical prote			
44	244	15.6	313	2	T25850	hypothetical prote			
45	241.5	15.5	358	2	T45944	hypothetical prote			
					ALIGNMENTS				

## RESULT 1

T07793 uncoupling protein (clone StUCP7), mitochondrial - potato

C;Species: Solanum tuberosum (potato)

C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000

C;Accession: T07793

R:Laloi, M.; Klein, M.; Riesmeier, J.W.; Mueller-Roeber, B.; Fleury, C.;

Bouliaud, F.; Ricquier, D.

Nature 389, 135-136, 1997

A;Title: A plant cold-induced uncoupling protein.

A;Reference number: 216136; PMID:9296489

A;Accession: T07793

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-306 <LAL>

A;Cross-references: EMBL:Y11220; PMID:92398828; PID:CAA72107.1; PID:92398829

A;Experimental source: cv. Desiree

C;Genetics:

A;Genome: nuclear

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: mitochondrial

Query Match 82.9%; Score 1294.5; DB 2; Length 306;

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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:12:22 ; Search time 10.613 Seconds

(without Alignments)

1486.693 Million cell updates/sec

Title: US-10-009-062-2

Perfect score: 1561

Sequence: 1 MGDHGPRTEISFGSSRAAF.....VIMFLTLEQVKKEFIKEVPN 303

Scoring table: BLOSUM62  
 GapPen 10.0 , Gapext 0.5

Searched: 141681 seqs. 52070155 residues

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	685.5	43.9	308	1	UCP3_MOUSE	P5501 mus musculus
2	684	43.8	311	1	UCP3_BOVIN	07792 bos taurus
3	684	43.8	311	1	UCP3_CANFA	Q92i3 canis familiaris
4	681.5	43.7	308	1	UCP3_RAT	P56499 rattus norvegicus
5	681.5	43.7	309	1	UCP2_PIG	09756 sus scrofa
6	680.5	43.6	309	1	UCP2_MOUSE	P70406 mus musculus
7	679.5	43.5	310	1	UCP2_CYPCA	Q9w725 cyprinus carpio
8	677.5	43.4	309	1	UCP2_RAT	P55500 rattus norvegicus
9	671.5	43.3	312	1	UCP3_HUMAN	P55916 homo sapiens
10	674.5	43.2	309	1	UCP2_HUMAN	P52851 homo sapiens
11	673.5	43.1	310	1	UCP2_BRAVE	Q9y720 brachydanio
12	669.5	42.9	308	1	UCP3_FIG	Q9649 sus scrofa
13	667.5	42.8	309	1	UCP2_CANFA	Q92i1 canis familiaris
14	613.5	39.3	307	1	UCP1_HUMAN	P28874 homo sapiens
15	591.5	37.9	306	1	UCP1_RAT	P0633 rattus norvegicus
16	589.5	37.8	306	1	UCP1_MOUSE	P12242 mus musculus
17	583.5	37.4	306	1	UCP1_MESEAU	P05575 mesocricetus auratus
18	579	37.1	306	1	UCP1_RABBIT	P14271 oryctolagus cuniculus

Search completed: May 18, 2004, 11:19:23  
 Job time : 11.613 secs

19	574	36.8	288	1	UCP1_BOVIN	P10861 bos taurus
20	524.5	33.6	323	1	UCP4_HUMAN	Q9547 homo sapiens
21	481	30.8	325	1	UCP5_MOUSE	Q9z2b2 mus musculus
22	478	30.6	325	1	Q2abx3	homo sapiens
23	447.5	28.7	287	1	DIC_HUMAN	Q9azd8 mus musculus
24	430	27.5	287	1	DIC_MOUSE	P22922 bos taurus
25	420	26.9	313	1	M2OM_BOVIN	Q9or62 mus musculus
26	419	26.8	313	1	M2OM_MOUSE	Q02978 homo sapiens
27	409	26.2	313	1	M2OM_HUMAN	P9700 rattus norvegicus
28	400	25.6	313	1	M2OM_RAT	P12332 saccharomyces cerevisiae
29	319	20.4	324	1	OACI_YEAST	P8mg98 mus musculus
30	302	19.3	322	1	SFC1_YEAST	P3303 saccharomyces cerevisiae
31	273	17.5	312	1	TXTP_CAEEL	Q9j19 caenorhabditis elegans
32	272.5	17.5	298	1	ODC_RAT	Q9jd3 rattus norvegicus
33	265.5	17.0	300	1	MCAT_ARATH	Q9xm7 arabidopsis thaliana
34	264	16.9	316	1	METC_MOUSE	Q9qgt8 homo sapiens
35	263.5	16.9	299	1	ODC_HUMAN	Q9jiso homo sapiens
36	263.5	16.9	675	1	CMC2_HUMAN	Q9hd1 homo sapiens
37	258.5	16.6	315	1	METC_HUMAN	Q9rxk4 mus musculus
38	257.5	16.5	676	1	CMC2_MOUSE	P50007 homo sapiens
39	257	16.5	311	1	TXTP_HUMAN	P32089 rattus norvegicus
40	257	16.5	311	1	TXTP_RAT	Q9j75 macaca fasciata
41	256.5	16.4	315	1	METC_MACPA	P31152 saccharomyces cerevisiae
42	253	16.2	299	1	TXTP_YEAST	P70110 bos taurus
43	253	16.2	311	1	TXTP_BOVIN	Q7546 homo sapiens
44	252	16.1	678	1	CNC1_HUMAN	P240556 saccharomyces cerevisiae

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#### OM protein - protein search, using SW model

Run on: May 18, 2004, 11:15:32 : Search time 38.2067 Seconds

(without alignments)

2502/2355 Million cell updates/sec

Title: US-10-009-962-2

Perfect score: 1561

Sequence: 1 MGDHGRTETISAGSSRAAF.....VIMFITLEQVKKKFIKEVEN 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 0

POST-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTRMBL\_25:\*
  - 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mtgc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rabbit:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_fruit:\*
  - 16: sp\_bacteriop:\*
  - 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	100.0	10	Q9MBE7	
2	89.0	10	Q8LNZ1	
3	86.1	10	Q9MBE6	
4	82.9	10	Q23391	
5	82.7	10	Q8FA58	
6	80.8	10	Q854C4	
7	79.0	10	Q81845	
8	78.4	10	Q65623	
9	77.5	10	Q8AVG1	
10	77.3	10	Q9ZNG1	
11	71.8	10	Q94F66	
12	71.2	10	Q8WIA4	
13	70.0	10	Q8WIA3	
14	69.9	10	Q9EXQ5	
15	69.4	10	Q9FXQ6	
16	69.0	10	Q9AVG2	
17	69.5	10	Q8TC50	
18	68.5	10	Q8BT99	
19	681.5	43.7	Q9D0T7	
20	680.5	43.6	Q9R446	
21	680.5	43.6	Q8CBU0	
22	679.5	43.5	Q9ERL7	
23	678.5	43.5	Q9DD07	
24	678.5	43.5	Q9D0T8	
25	678.5	43.5	Q7YVP4	
26	676.5	43.3	Q9R446	
27	675.5	43.3	Q8AYM4	
28	657.5	42.1	Q7ZKN1	
29	620	39.7	Q9GMZ1	
30	618	39.6	Q9XSE1	
31	615.5	39.4	Q7YRF2	
32	597.5	37.8	Q9ERL8	
33	583.5	37.4	Q8K404	
34	542	34.7	Q7T3F5	
35	530.5	34.0	Q9EPH7	
36	530.5	34.0	Q9D6D0	
37	522.5	33.9	Q8QG96	
38	520	33.3	Q8LDE6	
39	520	33.3	Q9SJ55	
40	511	32.7	Q9AK32	
41	510	32.7	Q9SB22	
42	508	32.5	Q9X1Z4	
43	505.5	32.4	Q84SBS	
44	503.5	32.3	Q9YX14	
45	499	32.0	Q9EPHS	

#### ALIGNMENTS

#### RESULT 1

ID	Q9MBE7	PRELIMINARY:	PRT;	303 AA.
AC	Q9MBE7;			
DT	01-OCT-2000 (TREMBLE1. 15, Created)			
DT	01-OCT-2000 (TREMBLE1. 15, Last sequence update)			
DT	01-OCT-2003 (TREMBLE1. 25, Last annotation update)			
DE	SFUCPA.			
GN	GN			

OS Symplocarpus renifolius.  
OC Eukaryota; Viridiplanteae; Stramenophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Araeaceae; Symplocarpaceae.  
OX NCBI\_TaxID=90003;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Ito K.;

RF "Isolation of two distinct cold-inducible cDNAs encoding plant uncoupling proteins from the spadix of skunk cabbage (Symplocarpus foetidus)." Plant Sci. 149:167-173 (1999).

RL CC |- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL: AB024723; BAA92172.1; -.  
DR GO: GO:0016021; C:internal to membrane; IEA.  
DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0005488; F:binding; IEA.  
DR GO: GO:0006839; P:mitochondrial transport; IEA.  
DR GO: GO:0006810; P:translocation; IEA.  
DR InterPro: IPR001993; Mitoch\_Carrier.  
DR InterPro: IPR002030; MitoC\_ uncoupling.  
DR PRINTS: PRO00784; MTUNCOPLING.  
DR PROSITE: PS00115; MTOCH\_CARRIER; 2.  
DR PROSITE; PS00115; MTOCH\_CARRIER; 2.  
KW Membrane; Transmembrane; 2.

SQ Sequence 303 AA; 32637 MN; FLE681CBB6EC3BBB3 CRC64;

Query Match 100.0%; Score 1561; DB 10; Length 303;  
Best Local Similarity 100.0%; Pred. No. 3..4e-126;  
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGDHGPTEISFAGSSRAAACFAELCTIPLDTAKVRLQLQQKAVTSDYVALFKYRCML 60  
Db 1 NGDGHPTEISFAGSSRAAACFAELCTIPLDTAKVRLQLQQKAVTSDYVALFKYRCML 60  
Qy 61 GTVATIAREGSLAWKGIVPGHLRQCLFGSLRGIGYBPVKSFYGVNIFYGDIPLSKKIL 120  
Db 61 GTVATIAREGSLAWKGIVPGHLRQCLFGSLRGIGYBPVKSFYGVNIFYGDIPLSKKIL 120  
Qy 121 AGLTGALIAIVANTPLDVKVRLQSEGKLPPGVRPYYRSCALNAYSTVKEGLCAWTGL 180  
Db 121 AGLTGALIAIVANTPLDVKVRLQSEGKLPPGVRPYYRSCALNAYSTVKEGLCAWTGL 180  
Qy 181 GPNTIARAIINAALASAYDQVKQTLLKPGFSNDIITHILAGAGFAVICGSPVDWIK 240  
Db 181 GPNTIARAIINAALASAYDQVKQTLLKPGFSNDIITHILAGAGFAVICGSPVDWIK 240  
Qy 241 SRMNGDSAYKSTPDCFIKTLDNLALFYKGFINFRGLGSWNTIMFTLQEVKFFIKE 300  
Db 241 SRMNGDSAYKSTPDCFIKTLDNLALFYKGFINFRGLGSWNTIMFTLQEVKFFIKE 300  
Qy 301 VPN 303  
Db 301 VPN 303

Search completed: May 18, 2004, 11:20:49  
Job time : 40.2067 secs